```
        10                  30                  50
        .   .   .   .   .   .   .   .   .   .   .   .
CAGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCC
        MetArgGlyThrProLysThrHisLeuLeuAlaPheSerLeuLeuCysLeuL
        70                  90                  110
        .   .   .   .   .   .   .   .   .   .   .   .
TCTCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCC
euSerLysValArgThrGlnLeuCysProThrProCysThrCysProTrpProProProA
        130                 150                 170
        .   .   .   .   .   .   .   .   .   .   .   .
GATGCCCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCAC
rgCysProLeuGlyValProLeuValLeuAspGlyCysGlyCysCysArgValCysAlaA
        190                 210                 230
        .   .   .   .   .   .   .   .   .   .   .   .
GGCGGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCT
rgArgLeuGlyGluProCysAspGlnLeuHisValCysAspAlaSerGlnGlyLeuValC
        250                 270                 290
        .   .   .   .   .   .   .   .   .   .   .   .
GCCAGCCCGGGGCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACA
ysGlnProGlyAlaGlyProGlyGlyArgGlyAlaLeuCysLeuLeuAlaGluAspAspS
        310                 330                 350
        .   .   .   .   .   .   .   .   .   .   .   .
GCAGCTGTGAGGTGAACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCA
erSerCysGluValAsnGlyArgLeuTyrArgGluGlyGluThrPheGlnProHisCysS
        370                 390                 410
        .   .   .   .   .   .   .   .   .   .   .   .
GCATCCGCTGCCGCTGCGAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATG
erIleArgCysArgCysGluAspGlyGlyPheThrCysValProLeuCysSerGluAspV
        430                 450                 470
        .   .   .   .   .   .   .   .   .   .   .   .
TGCGGCTGCCCAGCTGGGACTGCCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCT
alArgLeuProSerTrpAspCysProHisProArgArgValGluValLeuGlyLysCysC
        490                 510                 530
        .   .   .   .   .   .   .   .   .   .   .   .
GCCCTGAGTGGGTGTGCGGCCAAGGAGGGGGACTGGGGACCCAGCCCCTTCCAGCCCAAG
ysProGluTrpValCysGlyGlnGlyGlyGlyLeuGlyThrGlnProLeuProAlaGlnG
        550                 570                 590
        .   .   .   .   .   .   .   .   .   .   .   .
GACCCCAGTTTTCTGGCCTTGTCTCTTCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGA
lyProGlnPheSerGlyLeuValSerSerLeuProProGlyValProCysProGluTrpS
```

FIG. 1A

```
       610                  630                  650
        .    .    .    .    .    .    .    .    .    .
GCACGGCCTGGGGACCCTGCTCGACCACCTGTGGGCTGGGCATGGCCACCCGGGTGTCCA
erThrAlaTrpGlyProCysSerThrThrCysGlyLeuGlyMetAlaThrArgValSerA
       670                  690                  710
        .    .    .    .    .    .    .    .    .    .
ACCAGAACCGCTTCTGCCGACTGGAGACCCAGCGCCGCCTGTGCCTGTCCAGGCCCTGCC
snGlnAsnArgPheCysArgLeuGluThrGlnArgArgLeuCysLeuSerArgProCysP
       730                  750                  770
        .    .    .    .    .    .    .    .    .    .
CACCCTCCAGGGGTCGCAGTCCACAAAACAGTGCCTTCTAGAGCCGGGCTGGGAATGGGG
roProSerArgGlyArgSerProGlnAsnSerAlaPheEnd
       790                  810                  830
        .    .    .    .    .    .    .    .    .    .

ACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCCTGGGCCCTGGGCTGATGGAAGA
       850                  870                  890
        .    .    .    .    .    .    .    .    .    .
TGGTCCGTGCCCAGGCCCTTGGCTGCAGGCAACACTTTAGCTTGGGTCCACCATGCAGAA
       910                  930                  950
        .    .    .    .    .    .    .    .    .    .
CACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCGAGGTATGGCAGAGGTGCAAGA
       970                  990                 1010
        .    .    .    .    .    .    .    .    .    .
CCTAGTCCCCTTTCCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGTGTCCAGGGTCCTC
      1030                 1050                 1070
        .    .    .    .    .    .    .    .    .    .
TAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGGCGAGCTTTCT
      1090                 1110                 1130
        .    .    .    .    .    .    .    .    .    .
CTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGCTGCAGCA
      1150                 1170                 1190
        .    .    .    .    .    .    .    .    .    .
GGTGCTGGGCTGGACTGGCCATTTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAGAGAT
      1210                 1230                 1250
        .    .    .    .    .    .    .    .    .    .
TCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAAAATTGTTCCTGAATACAAGCCTATG
      1270
        .    .    .    .    .
CGTGAAAAAAAAAAAAAAAAAAAA
```

FIG. 1B

```
          1                                                  50

CTGF-1aa  MTAASMGPVR VAFVVLLALC SRPAV.GQNC SGPCRCPDEP APRCPAGVSL
CTGF-3aa  ....MRGTPK THLLAFSLLC LLSKVRTQLC PTPCTCP.WP PPRCPLGVPL

          51                                                 100
CTGF-1aa  VLDGCGCCRV CAKQLGELCT ERDPCDPHKG LFCDFGSPAN RKIGVC.TAK
CTGF-3aa  VLDGCGCCRV CARRLGEPCD QLHVCDASQG LVCQPGAGPG GRGALCLLAE

          101                                                150
CTGF-1aa  DGAPCIFGGT VYRSGESFQS SCKYQCTCLD GAVGCMPLCS MDVRLPSPDC
CTGF-3aa  DDSSCEVNGR LYREGETFQP HCSIRCRCED GGFTCVPLCS EDVRLPSWDC

          151                                                200
CTGF-1aa  PFPRRVKLPG KCCEEWVCDE PKDQTVVGPA LAAYRLEDTF GPDPTMIRAN
CTGF-3aa  PHPRRVEVLG KCCPEWVCGQ GGGLGTQPLP AQGPQFSGLV SSLPPGVP..

          201                                                250
CTGF-1aa  CLVQTTEWSA CSKTCGMGIS TRVTNDNASC RLEKQSRLCM VRPCEADLEE
CTGF-3aa  CPEWSTAWGP CSTTCGLGMA TRVSNQNRFC RLETQRRLCL SRPCPPSRGR

          251                                                300
CTGF-1aa  NIKKGKKCIR TPKISKPIKF ELSGCTSMKT YRAKFCGVCT DGRCCTPHRT
CTGF-3aa  SPQNSAF... .......... .......... .......... ..........

          301                                                350
CTGF-1aa  TTLPVEFKCP DGEVMKKNMM FIKTCACHYN CPGDNDIFES LYYRKMYGDM
CTGF-3aa  .......... .......... .......... .......... ..........

          351
CTGF-1aa  A
CTGF-3aa  .
```

FIG.2

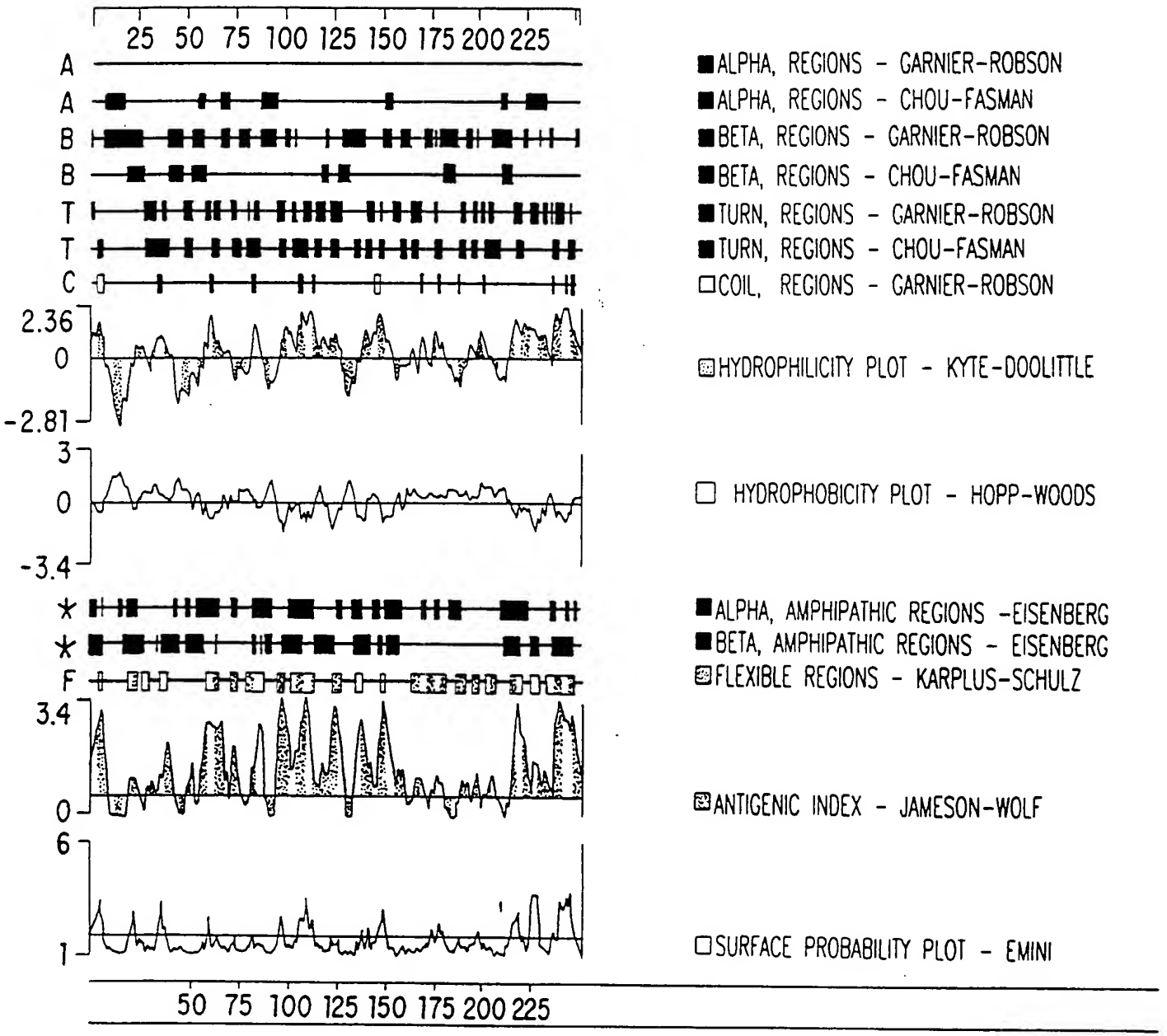
25 50 75 100 125 150 175 200 225
A
A
B
B
T
T
C
2.36
0
-2.81
3
0
-3.4
*
*
F
3.4
0
6
1
50 75 100 125 150 175 200 225
ALPHA, REGIONS - GARNIER-ROBSON
ALPHA, REGIONS - CHOU-FASMAN
BETA, REGIONS - GARNIER-ROBSON
BETA, REGIONS - CHOU-FASMAN
TURN, REGIONS - GARNIER-ROBSON
TURN, REGIONS - CHOU-FASMAN
COIL, REGIONS - GARNIER-ROBSON
HYDROPHILICITY PLOT - KYTE-DOOLITTLE
HYDROPHOBICITY PLOT - HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS -EISENBERG
BETA, AMPHIPATHIC REGIONS - EISENBERG
FLEXIBLE REGIONS - KARPLUS-SCHULZ
ANTIGENIC INDEX - JAMESON-WOLF
SURFACE PROBABILITY PLOT - EMINI

FIG.3